

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: <u>car</u>	NA Sequence (#) <u>✓</u>	STN _____	
Searcher Phone #: <u>2-2504</u>	AA Sequence (#) <u>✓</u>	Dialog _____	
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____	
Date Searcher Picked Up <u>1/8/05</u>	Bibliographic _____	Dr. Link _____	
Date Completed <u>1/8/05</u>	Litigation _____	Lexis/Nexis _____	
Searcher Prep. Review Time _____	Fulltext _____	Sequence Systems <u>✓</u>	
Clerical Prep. Time: <u>10</u>	Patent Family _____	WW/Internet _____	
Online Time <u>415</u>	Other _____	Other (specify) _____	



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 141839

TO: Ilia Ouspenski
Location: 3d74 / 3c70
Saturday, January 08, 2005
Art Unit: 1644
Phone: 272-2920
Serial Number: 10 / 008264

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1a51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes


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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Glimcher, L.H. and Szabo, S.J.
 TITLE T-bet compositions and methods of use thereof
 JOURNAL Patent: WO 0073453-A 3 07-DEC-2000,
 PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
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ORIGIN

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Best Local Similarity 85.7%; Pred. No. 1e-187;

Matches 1378; Conservative 0; Mismatches 215; Indels 15; Gaps 2;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 06:07:23 ; Search time 196 Seconds

(without alignments)
1570.538 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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9	943.5	32.1	688	2	Q9JTL1
10	937	31.8	661	2	Q9RTU2
11	937	31.8	661	2	Q9DDU3
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ALIGNMENTS

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
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RA Yang S.;
RT "Cloning and characterization of a new member of T-box gene family.";
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RA Szabo S.J., Kim S.T., Costa G.L., Zhang X., Fachman C.G.,
RA Glimcher L.H.;
RT "A novel transcription factor, T-bet, directs Th1 lineage commitment.";
RL Cell 100:655-669(2000).
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RA TISUE-Testis;
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RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Transcription factor that controls the expression of the Th1 cytokine, interferon-gamma. Initiates Th1 lineage development from naive Th precursor cells both by activating Th1 genetic

CC programs and by repressing the opposing TH2 programs.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: T-cell specific.
 CC -1- SIMILARITY: Contains 1 T-box domain.
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 CC This SMIS9-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@1sb-sib.ch).
 CC -----
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 DB OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 DB RA Zhang, Wx, Yang S.Y.;
 DB RT "Cloning and characterization of a new member of the T-box gene
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 DB RL Genomics 70:41-48(2000).
 DB RN [2]
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 DB RC STRAIN=BALB/c;
 DB RA Yang S.Y.
 DB RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DB DR EMBL; AF093099; AAF00056.1; -
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 DR Pfam; PF00907; T-box; 1.
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 DR SMART; SM00425; TBOX; 1.
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 DR PROSITE; PS01264; TBOX_2; 1.
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 CC 61 GALVPAAPSRFLGAVYPPRPOAAGPPGAGSPPPADAGYOPGEGYAAPDRAGLYPG 120
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 CC 61 GALVPAAPSRFLGAVYPPRPOAAGPPGAGSPPPADAGYOPGEGYAAPDRAGLYPG 120
 CC 61 GALVPAAPSRFLGAVYPPRPOAAGPPGAGSPPPADAGYOPGEGYAAPDRAGLYPG 120
 CC 121 PREDYALPAGLEYSGLKRLVANNHLLMSKFNQHOTEMIITKGRBMPFLSFTVAGLEPT 180
 CC 121 PREDYALPAGLEYSGLKRLVANNHLLMSKFNQHOTEMIITKGRBMPFLSFTVAGLEPT 180
 CC 121 PREDYALPAGLEYSGLKRLVANNHLLMSKFNQHOTEMIITKGRBMPFLSFTVAGLEPT 180
 CC 121 PREDYALPAGLEYSGLKRLVANNHLLMSKFNQHOTEMIITKGRBMPFLSFTVAGLEPT 180
 CC 181 SHTRMFVDVVLVDQHMRYOSGKRVOCGKAGSMPGNRLYVHDSPTNGAHMRRQVSVFG 240
 CC 181 SHTRMFVDVVLVDQHMRYOSGKRVOCGKAGSMPGNRLYVHDSPTNGAHMRRQVSVFG 240
 CC 181 SHTRMFVDVVLVDQHMRYOSGKRVOCGKAGSMPGNRLYVHDSPTNGAHMRRQVSVFG 240
 CC 181 SHTRMFVDVVLVDQHMRYOSGKRVOCGKAGSMPGNRLYVHDSPTNGAHMRRQVSVFG 240
 CC 241 KKLITNNKGSNNVTOMIVLQSLHKYQPRLIHYVNDGEBEACNANSTHITFTFOETQFI 300
 CC 241 KKLITNNKGSNNVTOMIVLQSLHKYQPRLIHYVNDGEBEACNANSTHITFTFOETQFI 300
 CC 241 KKLITNNKGSNNVTOMIVLQSLHKYQPRLIHYVNDGEBEACNANSTHITFTFOETQFI 300
 CC 241 KKLITNNKGSNNVTOMIVLQSLHKYQPRLIHYVNDGEBEACNANSTHITFTFOETQFI 300
 CC 301 AATAYQNAEITQKIDNNPPAKGFRENFSNMTSVDTSPSPGPNCOFLGSDHYSPILP 360
 CC 301 AATAYQNAEITQKIDNNPPAKGFRENFSNMTSVDTSPSPGPNCOFLGSDHYSPILP 360
 CC 301 AATAYQNAEITQKIDNNPPAKGFRENFSNMTSVDTSPSPGPNCOFLGSDHYSPILP 360
 CC 301 AATAYQNAEITQKIDNNPPAKGFRENFSNMTSVDTSPSPGPNCOFLGSDHYSPILP 360
 CC 421 RQGEVLAEGAGWPAAPYPPKMGASFRPMTLPMKPGGSGSGRPEOQGLVWTEI 480
 CC 421 RQGEVLAEGAGWPAAPYPPKMGASFRPMTLPMKPGGSGSGRPEOQGLVWTEI 480
 CC 421 RQGEVLAEGAGWPAAPYPPKMGASFRPMTLPMKPGGSGSGRPEOQGLVWTEI 480
 CC 421 RQGEVLAEGAGWPAAPYPPKMGASFRPMTLPMKPGGSGSGRPEOQGLVWTEI 480
 CC 481 APTRPSSDSGLGKSDSKRRRVSPYPSGDSPPAGAPSPFDKEABQFYNYFPN 535
 CC 481 APTRPSSDSGLGKSDSKRRRVSPYPSGDSPPAGAPSPFDKEABQFYNYFPN 535